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Sequence Listing was accepted.

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Reviewer: Durreshwar Anjum

Timestamp: [year=2009; month=1; day=4; hr=16; min=35; sec=46; ms=378; ]

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Application No: 10561867 Version No: 3.0

Input Set:

Output Set:

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Finished: 2008-12-22 16:23:04.277  
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Total Warnings: 5  
Total Errors: 0  
No. of SeqIDs Defined: 7  
Actual SeqID Count: 7

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# SEQUENCE LISTING

<110> BURNOUF, Dominique, Yves, Joel  
 WAGNER, Jerome, Edouard  
 DUMAS, Philippe  
 FUJII, Shingo  
 FUCHS, Robert, Pierre, Paul  
 OLIERIC, Vincent

<120> PROTEIN CRYSTAL COMPRISING THE PROCESSIVITY CLAMP FACTOR  
 OF DNA POLYMERASE AND A LIGAND, AND ITS USES

<130> 0508-1147

<140> 10561867

<141> 2008-12-22

<150> PCT/EP2004/006942

<151> 2004-06-25

<150> EP 03291596.9

<151> 2003-06-27

<160> 7

<170> PatentIn version 3.5

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<211> 16

<212> PRT

<213> Escherichia coli

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<210> 2

<211> 22

<212> PRT

<213> Artificial sequence

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<223> synthetic peptide

<400> 2

Arg	Pro	Val	Lys	Val	Thr	Pro	Asn	Gly	Ala	Glu	Asp	Glu	Ser	Ala	Glu
1				5					10					15	

Ala	Phe	Pro	Leu	Glu	Phe
				20	

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 <223> synthetic oligonucleotide - Primer for replication assay  
  
 <400> 3  
 gtaaaacgac ggccagtgcc aagcttagtc 30

<210> 4  
 <211> 90  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> synthetic oligonucleotide - template for replication assay  
  
 <400> 4  
 ccatgattac gaattcagtc atcacggcg ccacagacta agcttggcac tggccgtcgt 60  
  
 tttaaacgt cgtgactggg aaaaccctgg 90

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 <211> 366  
 <212> PRT  
 <213> Escherichia coli  
  
 <400> 5

Met Lys Phe Thr Val Glu Arg Glu His Leu Leu Lys Pro Leu Gln Gln  
 1 5 10 15

Val Ser Gly Pro Leu Gly Gly Arg Pro Thr Leu Pro Ile Leu Gly Asn  
 20 25 30

Leu Leu Leu Gln Val Ala Asp Gly Thr Leu Ser Leu Thr Gly Thr Asp  
 35 40 45

Leu Glu Met Glu Met Val Ala Arg Val Ala Leu Val Gln Pro His Glu  
 50 55 60

Pro Gly Ala Thr Thr Val Pro Ala Arg Lys Phe Phe Asp Ile Cys Arg  
 65 70 75 80

Gly Leu Pro Glu Gly Ala Glu Ile Ala Val Gln Leu Glu Gly Glu Arg  
 85 90 95

Met Leu Val Arg Ser Gly Arg Ser Arg Phe Ser Leu Ser Thr Leu Pro  
100 105 110

Ala Ala Asp Phe Pro Asn Leu Asp Asp Trp Gln Ser Glu Val Glu Phe  
115 120 125

Thr Leu Pro Gln Ala Thr Met Lys Arg Leu Ile Glu Ala Thr Gln Phe  
130 135 140

Ser Met Ala His Gln Asp Val Arg Tyr Tyr Leu Asn Gly Met Leu Phe  
145 150 155 160

Glu Thr Glu Gly Glu Glu Leu Arg Thr Val Ala Thr Asp Gly His Arg  
165 170 175

Leu Ala Val Cys Ser Met Pro Ile Gly Gln Ser Leu Pro Ser His Ser  
180 185 190

Val Ile Val Pro Arg Lys Gly Val Ile Glu Leu Met Arg Met Leu Asp  
195 200 205

Gly Gly Asp Asn Pro Leu Arg Val Gln Ile Gly Ser Asn Asn Ile Arg  
210 215 220

Ala His Val Gly Asp Phe Ile Phe Thr Ser Lys Leu Val Asp Gly Arg  
225 230 235 240

Phe Pro Asp Tyr Arg Arg Val Leu Pro Lys Asn Pro Asp Lys His Leu  
245 250 255

Glu Ala Gly Cys Asp Leu Leu Lys Gln Ala Phe Ala Arg Ala Ala Ile  
260 265 270

Leu Ser Asn Glu Lys Phe Arg Gly Val Arg Leu Tyr Val Ser Glu Asn  
275 280 285

Gln Leu Lys Ile Thr Ala Asn Asn Pro Glu Gln Glu Glu Ala Glu Glu  
290 295 300

Ile Leu Asp Val Thr Tyr Ser Gly Ala Glu Met Glu Ile Gly Phe Asn  
305 310 315 320

Val Ser Tyr Val Leu Asp Val Leu Asn Ala Leu Lys Cys Glu Asn Val

325

330

335

Arg Met Met Leu Thr Asp Ser Val Ser Ser Val Gln Ile Glu Asp Ala  
340 345 350

Ala Ser Gln Ser Ala Ala Tyr Val Val Met Pro Met Arg Leu  
355 360 365

&lt;210&gt; 6

&lt;211&gt; 7

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetic peptide - derived from SEQ ID NO 1

&lt;400&gt; 6

Arg Gln Leu Val Leu Gly Leu  
1 5

&lt;210&gt; 7

&lt;211&gt; 210

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> synthetic peptide - derived from beta clamp of  
E. coli DNA polymerase III

&lt;400&gt; 7

Leu Asn Gly Met Leu Phe Glu Thr Glu Gly Glu Glu Leu Arg Thr Val  
1 5 10 15

Ala Thr Asp Gly His Arg Leu Ala Val Cys Ser Met Pro Ile Gly Gln  
20 25 30

Ser Leu Pro Ser His Ser Val Ile Val Pro Arg Lys Gly Val Ile Glu  
35 40 45

Leu Met Arg Met Leu Asp Gly Gly Asp Asn Pro Leu Arg Val Gln Ile  
50 55 60

Gly Ser Asn Asn Ile Arg Ala His Val Gly Asp Phe Ile Phe Thr Ser  
65 70 75 80

Lys Leu Val Asp Gly Arg Phe Pro Asp Tyr Arg Arg Val Leu Pro Lys

85

90

95

Asn Pro Asp Lys His Leu Glu Ala Gly Cys Asp Leu Leu Lys Gln Ala  
100 105 110

Phe Ala Arg Ala Ala Ile Leu Ser Asn Glu Lys Phe Arg Gly Val Arg  
115 120 125

Leu Tyr Val Ser Glu Asn Gln Leu Lys Ile Thr Ala Asn Asn Pro Glu  
130 135 140

Gln Glu Glu Ala Glu Glu Ile Leu Asp Val Thr Tyr Ser Gly Ala Glu  
145 150 155 160

Met Glu Ile Gly Phe Asn Val Ser Tyr Val Leu Asp Val Leu Asn Ala  
165 170 175

Leu Lys Cys Glu Asn Val Arg Met Met Leu Thr Asp Ser Val Ser Ser  
180 185 190

Val Gln Ile Glu Asp Ala Ala Ser Gln Ser Ala Ala Tyr Val Val Met  
195 200 205

Pro Met  
210